

## LIST OF SEQUENCES

<110> Assistance Publique - Hôpitaux de Paris (AH-HP)  
 Institut National de la Santé et de la recherche Médicale  
 (INSERM)  
 Institut Gustave Roussy (IGR)  
 Université de Versailles - Saint-Quentin-en-Yvelines  
 Université Paris-Sud

<120> Identification of a JAK2 mutation involved in Vaquez  
 Polyglobulia

<130> D 22 707 / 241 699

<140> FR04-11480  
<141> 2004-10-27

<160> 31

<170> PatentIn Ver. 3.3

<210> 1  
<211> 1132  
<212> PRT  
<213> homo sapiens

<220>  
<223> variant JAK2 V617F.

<400> 1

Met	Gly	Met	Ala	Cys	Leu	Thr	Met	Thr	Glu	Met	Glu	Gly	Thr	Ser	Thr
1					5				10					15	

Ser	Ser	Ile	Tyr	Gln	Asn	Gly	Asp	Ile	Ser	Gly	Asn	Ala	Asn	Ser	Met
					20			25					30		

Lys	Gln	Ile	Asp	Pro	Val	Leu	Gln	Val	Tyr	Leu	Tyr	His	Ser	Leu	Gly
						35		40				45			

Lys	Ser	Glu	Ala	Asp	Tyr	Leu	Thr	Phe	Pro	Ser	Gly	Glu	Tyr	Val	Ala
					50			55				60			

Glu	Glu	Ile	Cys	Ile	Ala	Ala	Ser	Lys	Ala	Cys	Gly	Ile	Thr	Pro	Val
65								70		75			80		

Tyr	His	Asn	Met	Phe	Ala	Leu	Met	Ser	Glu	Thr	Glu	Arg	Ile	Trp	Tyr
						85			90			95			

Pro	Pro	Asn	His	Val	Phe	His	Ile	Asp	Glu	Ser	Thr	Arg	His	Asn	Val
						100			105			110			

Leu	Tyr	Arg	Ile	Arg	Phe	Tyr	Phe	Pro	Arg	Trp	Tyr	Cys	Ser	Gly	Ser
						115		120				125			

Asn	Arg	Ala	Tyr	Arg	His	Gly	Ile	Ser	Arg	Gly	Ala	Glu	Ala	Pro	Leu
						130		135				140			

Leu	Asp	Asp	Phe	Val	Met	Ser	Tyr	Leu	Phe	Ala	Gln	Trp	Arg	His	Asp
						145		150				155		160	

Phe Val His Gly Trp Ile Lys Val Pro Val Thr His Glu Thr Gln Glu  
 165 170 175  
 Glu Cys Leu Gly Met Ala Val Leu Asp Met Met Arg Ile Ala Lys Glu  
 180 185 190  
 Asn Asp Gln Thr Pro Leu Ala Ile Tyr Asn Ser Ile Ser Tyr Lys Thr  
 195 200 205  
 Phe Leu Pro Lys Cys Ile Arg Ala Lys Ile Gln Asp Tyr His Ile Leu  
 210 215 220  
 Thr Arg Lys Arg Ile Arg Tyr Arg Phe Arg Arg Phe Ile Gln Gln Phe  
 225 230 235 240  
 Ser Gln Cys Lys Ala Thr Ala Arg Asn Leu Lys Leu Lys Tyr Leu Ile  
 245 250 255  
 Asn Leu Glu Thr Leu Gln Ser Ala Phe Tyr Thr Glu Lys Phe Glu Val  
 260 265 270  
 Lys Glu Pro Gly Ser Gly Pro Ser Gly Glu Glu Ile Phe Ala Thr Ile  
 275 280 285  
 Ile Ile Thr Gly Asn Gly Gly Ile Gln Trp Ser Arg Gly Lys His Lys  
 290 295 300  
 Glu Ser Glu Thr Leu Thr Glu Gln Asp Leu Gln Leu Tyr Cys Asp Phe  
 305 310 315 320  
 Pro Asn Ile Ile Asp Val Ser Ile Lys Gln Ala Asn Gln Glu Gly Ser  
 325 330 335  
 Asn Glu Ser Arg Val Val Thr Ile His Lys Gln Asp Gly Lys Asn Leu  
 340 345 350  
 Glu Ile Glu Leu Ser Ser Leu Arg Glu Ala Leu Ser Phe Val Ser Leu  
 355 360 365  
 Ile Asp Gly Tyr Tyr Arg Leu Thr Ala Asp Ala His His Tyr Leu Cys  
 370 375 380  
 Lys Glu Val Ala Pro Pro Ala Val Leu Glu Asn Ile Gln Ser Asn Cys  
 385 390 395 400  
 His Gly Pro Ile Ser Met Asp Phe Ala Ile Ser Lys Leu Lys Lys Ala  
 405 410 415  
 Gly Asn Gln Thr Gly Leu Tyr Val Leu Arg Cys Ser Pro Lys Asp Phe  
 420 425 430  
 Asn Lys Tyr Phe Leu Thr Phe Ala Val Glu Arg Glu Asn Val Ile Glu  
 435 440 445  
 Tyr Lys His Cys Leu Ile Thr Lys Asn Glu Asn Glu Glu Tyr Asn Leu  
 450 455 460  
 Ser Gly Thr Lys Lys Asn Phe Ser Ser Leu Lys Asp Leu Leu Asn Cys  
 465 470 475 480

Tyr Gln Met Glu Thr Val Arg Ser Asp Asn Ile Ile Phe Gln Phe Thr  
 485 490 495  
 Lys Cys Cys Pro Pro Lys Pro Lys Asp Lys Ser Asn Leu Leu Val Phe  
 500 505 510  
 Arg Thr Asn Gly Val Ser Asp Val Pro Thr Ser Pro Thr Leu Gln Arg  
 515 520 525  
 Pro Thr His Met Asn Gln Met Val Phe His Lys Ile Arg Asn Glu Asp  
 530 535 540  
 Leu Ile Phe Asn Glu Ser Leu Gly Gln Gly Thr Phe Thr Lys Ile Phe  
 545 550 555 560  
 Lys Gly Val Arg Arg Glu Val Gly Asp Tyr Gly Gln Leu His Glu Thr  
 565 570 575  
 Glu Val Leu Leu Lys Val Leu Asp Lys Ala His Arg Asn Tyr Ser Glu  
 580 585 590  
 Ser Phe Phe Glu Ala Ala Ser Met Met Ser Lys Leu Ser His Lys His  
 595 600 605  
 Leu Val Leu Asn Tyr Gly Val Cys Phe Cys Gly Asp Glu Asn Ile Leu  
 610 615 620  
 Val Gln Glu Phe Val Lys Phe Gly Ser Leu Asp Thr Tyr Leu Lys Lys  
 625 630 635 640  
 Asn Lys Asn Cys Ile Asn Ile Leu Trp Lys Leu Glu Val Ala Lys Gln  
 645 650 655  
 Leu Ala Trp Ala Met His Phe Leu Glu Glu Asn Thr Leu Ile His Gly  
 660 665 670  
 Asn Val Cys Ala Lys Asn Ile Leu Leu Ile Arg Glu Glu Asp Arg Lys  
 675 680 685  
 Thr Gly Asn Pro Pro Phe Ile Lys Leu Ser Asp Pro Gly Ile Ser Ile  
 690 695 700  
 Thr Val Leu Pro Lys Asp Ile Leu Gln Glu Arg Ile Pro Trp Val Pro  
 705 710 715 720  
 Pro Glu Cys Ile Glu Asn Pro Lys Asn Leu Asn Leu Ala Thr Asp Lys  
 725 730 735  
 Trp Ser Phe Gly Thr Thr Leu Trp Glu Ile Cys Ser Gly Gly Asp Lys  
 740 745 750  
 Pro Leu Ser Ala Leu Asp Ser Gln Arg Lys Leu Gln Phe Tyr Glu Asp  
 755 760 765  
 Arg His Gln Leu Pro Ala Pro Lys Trp Ala Glu Leu Ala Asn Leu Ile  
 770 775 780  
 Asn Asn Cys Met Asp Tyr Glu Pro Asp Phe Arg Pro Ser Phe Arg Ala  
 785 790 795 800  
 Ile Ile Arg Asp Leu Asn Ser Leu Phe Thr Pro Asp Tyr Glu Leu Leu

805	810	815
Thr Glu Asn Asp Met Leu Pro Asn Met Arg Ile Gly Ala Leu Gly Phe		
820	825	830
Ser Gly Ala Phe Glu Asp Arg Asp Pro Thr Gln Phe Glu Glu Arg His		
835	840	845
Leu Lys Phe Leu Gln Gln Leu Gly Lys Gly Asn Phe Gly Ser Val Glu		
850	855	860
Met Cys Arg Tyr Asp Pro Leu Gln Asp Asn Thr Gly Glu Val Val Ala		
865	870	875
Val Lys Lys Leu Gln His Ser Thr Glu Glu His Leu Arg Asp Phe Glu		
885	890	895
Arg Glu Ile Glu Ile Leu Lys Ser Leu Gln His Asp Asn Ile Val Lys		
900	905	910
Tyr Lys Gly Val Cys Tyr Ser Ala Gly Arg Arg Asn Leu Lys Leu Ile		
915	920	925
Met Glu Tyr Leu Pro Tyr Gly Ser Leu Arg Asp Tyr Leu Gln Lys His		
930	935	940
Lys Glu Arg Ile Asp His Ile Lys Leu Leu Gln Tyr Thr Ser Gln Ile		
945	950	955
960		
Cys Lys Gly Met Glu Tyr Leu Gly Thr Lys Arg Tyr Ile His Arg Asp		
965	970	975
Leu Ala Thr Arg Asn Ile Leu Val Glu Asn Glu Asn Arg Val Lys Ile		
980	985	990
Gly Asp Phe Gly Leu Thr Lys Val Leu Pro Gln Asp Lys Glu Tyr Tyr		
995	1000	1005
Lys Val Lys Glu Pro Gly Glu Ser Pro Ile Phe Trp Tyr Ala Pro		
1010	1015	1020
Glu Ser Leu Thr Glu Ser Lys Phe Ser Val Ala Ser Asp Val Trp		
1025	1030	1035
Ser Phe Gly Val Val Leu Tyr Glu Leu Phe Thr Tyr Ile Glu Lys		
1040	1045	1050
Ser Lys Ser Pro Pro Ala Glu Phe Met Arg Met Ile Gly Asn Asp		
1055	1060	1065
Lys Gln Gly Gln Met Ile Val Phe His Leu Ile Glu Leu Leu Lys		
1070	1075	1080
Asn Asn Gly Arg Leu Pro Arg Pro Asp Gly Cys Pro Asp Glu Ile		
1085	1090	1095
Tyr Met Ile Met Thr Glu Cys Trp Asn Asn Asn Val Asn Gln Arg		
1100	1105	1110
Pro Ser Phe Arg Asp Leu Ala Leu Arg Val Asp Gln Ile Arg Asp		
1115	1120	1125

Asn Met Ala Gly  
1130

<210> 2  
<211> 5097  
<212> DNA  
<213> homo sapiens

<220>  
<223> G18497 mutation in jak2 gene

<400> 2		
ctgcaggaag gagagaggaa gaggagcaga agggggcagc agcggacgcc gctaacggcc	60	
tccctcgccg ctgacaggct gggccggcgc ccggctcgct tgggtgttcg cgtcgccact	120	
tcggcttctc ggccgggtcgg gcccctcggc ccgggcttgc ggccgcgcgtc ggggctgagg	180	
gctgctgcgg cgcagggaga ggcctggtcc tcgctgccga gggatgtgag tgggagctga	240	
gcccacactg gaggggcccc gaggggcccaag cctggaggtc gttcagagcc gtgcccgc	300	
cggggcttcg cagaccttga cccgggggtt aggagccgccc cctgccccgt cgagggcg	360	
ctctggtcgc ccgatctgtg tagccggttt cagaaggcagg caacaggaac aagatgtgaa	420	
ctgtttctct tctgcagaaa aagaggctct tcctcctcct cccgcacgg caaatgttct	480	
aaaaaaagact ctgcatggga atggcctgcc ttacgatgac agaaatggag ggaacatcca	540	
cctcttctat atatcagaat ggtgatattt ctggaaatgc caattctatg aagcaaata	600	
atccagttct tcaggtgtat cttaaccatt cccttggaa atctgaggca gattatctga	660	
cctttccatc tggggagttt gttcagaag aaatctgtat tgctgcttct aaagcttgc	720	
gtatcacacc tgtgtatcat aatatgttg cttaatgag tgaaacagaa agatctgg	780	
atccacccaa ccatgtcttc catatagatg agtcaaccag gcataatgta ctctacagaa	840	
taagatttta ctccctcgt tggatttgcgt gtggcagca cagagcctat cggcatggaa	900	
tatctcgagg tgctgaagct cctcttcttgc atgactttgt catgttttac ctcttgc	960	
agtggcggca tgattttgtt cacggatgga taaaagtacc tgtgactcat gaaacacagg	1020	
aagaatgtct tgggatggca gtgttagata tggatgaaat agccaaagaa aacgatcaa	1080	
ccccactggc catctataac tctatcagct acaagacatt cttacaaaaa tgtattcgag	1140	
caaagatcca agactatcat attttgacaa ggaagcgaat aaggtacaga ttgcgcagat	1200	
ttattcagca attcagccaa tgcaaagcca ctgccagaaa cttgaaactt aagtatctt	1260	
taaatctgga aactctgcag tctgccttct acacagagaa atttgaagta aaagaacctg	1320	
gaagtggtcc ttccagggtgag gagatttttgc accattat aataactgga aacggtgaa	1380	
ttcagggtgc aagaggaaa cataaagaaa gtgagacact gacagaacag gatttacagt	1440	

tatattgcga tttcctaatttattgtatcgatattaa gcaagcaaac caagagggtt	1500
caaataatgaaag ccgagttgtactatccata agcaagatgg taaaatctg gaaattgaac	1560
tttagctcatt aaggaaagct ttgtcttcgttgtcattaat tgatggatat tatagattaa	1620
ctgcagatgc acatcattac ctctgtaaag aagtagcacc tccagccgtg cttgaaaata	1680
tacaaagcaa ctgtcatggc ccaatttcga tgatTTTgc cattagtaaa ctgaagaaag	1740
caggtaatca gactggactg tatgtacttc gatgcagtcc taaggacttt aataaatatt	1800
ttttgacttt tgctgtcgag cgagaaaaatg tcattgaata taaacactgt ttgattacaa	1860
aaaatgagaa tgaagagtac aacctcagtg ggacaaagaa gaacttcagc agtcttaaag	1920
atctttgaa ttgttaccag atggaaactg ttgcgtcaga caatataatt ttccagttta	1980
ctaaatgctg tcccccaaag ccaaaagata aatcaaacct tctagtcttc agaacgaatg	2040
gtgtttctga tgtaccaacc tcaccaacat tacagaggcc tactcatatg aaccaaatgg	2100
tgtttcacaa aatcagaaat gaagatttga tatttaatga aagccttggc caaggcactt	2160
ttacaaagat tttaaaggc gtacgaagag aagtaggaga ctacggtaa ctgcataaaa	2220
cagaagttct tttaaaagtt ctggataaaag cacacagaaa ctattcagag tctttcttg	2280
aagcagcaag tatgtatgagc aagctttc acaagcattt ggttttaaat tatggagtat	2340
gtttctgtgg agacgagaat attctgtttc aggagttgt aaaatttggta tcaactagata	2400
catatctgaa aaagaataaa aattgtataa atatattatg gaaacttgaa gttgctaaac	2460
agttggcatg ggccatgcat tttctagaag aaaacaccct tattcatggg aatgtatgt	2520
ccaaaaat tctgcttac agagaagaag acaggaagac aggaaatcct cctttcatca	2580
aacttagtga tcctggcatt agtattacag tttgccaaa ggacattttt caggagagaa	2640
taccatgggt accacctgaa tgcattgaaa atcctaaaaa tttaatttgc gcaacagaca	2700
aatggagtt tggttaccact ttgtggaaa tctgcagtgg aggagataaa cctctaagt	2760
ctctggattc tcaaagaaag ctacaattttt atgaagatag gcatcagctt cctgcaccaa	2820
agtgggcaga attagcaaacc tttataaata attgtatggat tattgaacca gatttcaggc	2880
cttctttcag agccatcata cgagatcttta acagttgtt tactccagat tatgaactat	2940
taacagaaaa tgacatgtta ccaaataatga ggataggtgc cctagggttt tctggtgct	3000
ttgaagaccg ggatcctaca cagtttgaag agagacattt gaaatttcta cagcaacttgc	3060
gcaagggtaa ttttggagt gtggagatgt gccggatgatga ccctctacag gacaacactg	3120
gggaggttgtt cgctgtaaaa aagcttcagc atagttactga agagcaccta agagacttt	3180
aaaggaaat tgaatccctg aaatccctac agcatgacaa cattgtaaag tacaagggag	3240

tgtgctacag tgctggtcgg cgtaatctaa aattaattat ggaatattta ccatatggaa	3300
gtttacgaga ctatctcaa aaacataaaag aacggataga tcacataaaa cttctgcagt	3360
acacatctca gatatgcaag ggtatggagt atcttggtag aaaaaggat atccacaggg	3420
atctggcaac gagaaatata ttggtgaga acgagaacag agttaaaatt ggagattttg	3480
ggttaaccaa agtcttgcca caagacaaag aatactataa agtaaaagaa cctggtgaaa	3540
gtcccatatt ctggtatgct ccagaatcac tgacagagag caagtttct gtggcctcag	3600
atgtttggag ctttggagtg gttctgtatg aactttcac atacatttag aagagtaaaa	3660
gtccaccagc ggaattttag cgtatgattt gcaatgacaa acaaggacag atgatcgtgt	3720
tccatttgat agaactttt aagaataatg gaagattacc aagaccagat ggatgccag	3780
atgagatcta tatgatcatg acagaatgct ggaacaataa tgtaaatcaa cgccccctcct	3840
ttagggatct agctttcgta gtggatcaaa taaggataa catggctgga taaaagaaat	3900
gaccttcatt ctgagaccaa agtagattt cagaacaaag ttttatattt cacattgctg	3960
tggactatta ttacatatata cattattata taaatcatga tgctagccag caaagatgt	4020
aaaatatctg ctcaaaactt tcaaagttt gtaagtttt cttcatgagg ccaccagtaa	4080
aagacattaa tgagaattcc ttagcaagga tttttaaga agtttcttaa acattgtctg	4140
ttaacatcac tcttgtctgg caaaagaaaa aaaatagact tttcaactc agcttttga	4200
gacctgaaaa aattattatg taaattttgc aatgttaaag atgcacagaa tatgtatgt	4260
tagttttac cacagtggat gtataatacc ttggcatctt gtgtgatgtt ttacacacat	4320
gagggctggt gttcattaat actgtttct aattttcca tagtaatct ataattaatt	4380
acttcactat acaaacaaat taagatgttc agataattga ataagtacct ttgtgtcctt	4440
gttcatttat atcgctggcc agcattataa gcaggtgtat acttttagct tgttagttcca	4500
tgtactgtaa atattttca cataaaggaa acaaatgtct agttttattt gtataggaaa	4560
ttccctgac cctaaataat acattttgaa atgaaacaag cttacaaaga tataatctat	4620
tttattatgg ttcccttgt atctatttg ggtgaatgtg tttttaaat ggaactatct	4680
ccaaattttt ctaagactac tatgaacagt tttctttaa aattttgaga ttaagaatgc	4740
caggaatatt gtcacccctt gagctgctga ctgccaataa cattcttcga tctctggat	4800
ttatgctcat gaactaaatt taagcttaag ccataaaata gattagattg tttttaaaa	4860
atggatagct cattaagaag tgcagcaggt taagaatttt ttcctaaaga ctgtatattt	4920
gaggggtttc agaattttgc attgcagtca tagaagagat ttatccctt ttttagaggg	4980
aaatgaggtt aataagtaaa aaagtatgct tgttaattt attcaagaat gccagtagaa	5040
aattcataac gtgtatctt aagaaaaatg agcatacacatc ttaaatctt tcaatta	5097

<210> 3  
 <211> 554  
 <212> DNA  
 <213> homo sapiens

<220>  
 <223> fragment of SEQ ID N°2 with the G1849T mutation

<400> 3	
ctcatatgaa ccaaatggtg tttcacaaaa tcagaaatga agatttgata ttatgaaa	60
gccttggcca aggactttt acaaagattt ttaaaggcgt acgaagagaa gtaggagact	120
acggtcaact gcatgaaaca gaagttctt taaaagttct ggataaagca cacagaaact	180
attcagagtc ttctttgaa gcagcaagta tgatgagcaa gctttctcac aagcatttgg	240
ttttaaatta tggagtatgt ttctgtggag acgagaatat tctggttcag gagtttgtaa	300
aatttggatc actagataca tatctgaaaaa agaataaaaaa ttgtataaat atattatgga	360
aacttgaagt tgctaaacag ttggcatggg ccatgcattt tctagaagaa aacaccctta	420
ttcatggaa tgtatgtgcc aaaaatattc tgcttatcag agaagaagac aggaagacag	480
gaaatcctcc ttcatcaaa cttagtgatc ctggcattag tattacagtt ttgccaaagg	540
acattcttca ggag	554

<210> 4  
 <211> 94  
 <212> DNA  
 <213> homo sapiens

<220>  
 <223> fragment of SEQ ID N°3 with the G1849T mutation

<400> 4	
gatgagcaag ctttctcaca agcatttgggt tttaaattttt ggagtatgtt tctgtggaga	60
cgagaatattt ctggttcagg agtttgtaaa attt	94

<210> 5  
 <211> 20  
 <212> DNA  
 <213> Artificial sequence

<220>  
 <223> PCR PRIMER (54804-54823)

<400> 5	
gggtttcctc agaacgttga	20

<210> 6

<211> 21  
<212> DNA  
<213> Artificial sequence

<220>  
<223> PCR PRIMER (55240-55260)

<400> 6  
ttgcttcct tttcacaag a 21

<210> 7  
<211> 20  
<212> DNA  
<213> Artificial sequence

<220>  
<223> SEQUENCING PRIMER (54813-54832)

<400> 7  
cagaacgttg atggcagttg 20

<210> 8  
<211> 27  
<212> DNA  
<213> Artificial sequence

<220>  
<223> SEQUENCING PRIMER (55207-55233)

<400> 8  
tgaatagtcc tacagtgtt tcagttt 27

<210> 9  
<211> 21  
<212> DNA  
<213> Artificial sequence

<220>  
<223> PCR AND SEQUENCING PRIMER (1386-1407)

<400> 9  
caacctcagt gggacaaaaga a 21

<210> 10  
<211> 23  
<212> DNA  
<213> Artificial sequence

<220>  
<223> PCR AND SEQUENCING PRIMER (2019-2041)

<400> 10  
gcagaatatt ttggcacat aca 23

<210> 11  
<211> 42

```

<212> DNA
<213> Artificial sequence

<220>
<223> SNPS PROBES AND DETECTION OF MUTATION AND siRNA (1829-1870)

<400> 11
ttttaaatta tggagtatgt gtctgtggag acgagaatat tc          42

<210> 12
<211> 23
<212> DNA
<213> homo sapiens

<220>
<223> Sequence comprising the G1849T mutation

<400> 12
tatggagtagt gtttctgtgg aga          23

<210> 13
<211> 21
<212> RNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (20)..(21)
<223> n is T

<220>
<223> sense siRNA

<400> 13
uggaguaugu uucuguggan n          21

<210> 14
<211> 21
<212> RNA
<213> homo sapiens

<220>
<221> misc_feature
<222> (20)..(21)
<223> n is T

<220>
<223> antisense siRNA

<400> 14
uccacagaaa cauacuccan n          21

<210> 15
<211> 21

```

<212> DNA		
<213> Artificial sequence		
<220>		
<223> Oligo "S" (sense)		
<400> 15		
ggcagagaga attttctgaa c		21
<210> 16		
<211> 21		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Oligo "R" (antisense)		
<400> 16		
gttttccttt ttcacaagat a		21
<210> 17		
<211> 25		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> "Sensor wt"		
<400> 17		
gtctccacag acacatactc cataa		25
<210> 18		
<211> 25		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> JAK2 primer		
<400> 18		
aaaacccaaat gcttgatgaa aagct		25
<210> 19		
<211> 23		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> cJAK2F		
<400> 19		
gcacacagaa actattcaga gtc		23
<210> 20		
<211> 19		
<212> DNA		

<213> Artificial sequence	
<220>	
<223> cJAK2S	
<400> 20	
agcagcaagt atgatgagc	19
<210> 21	
<211> 24	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> cJAK2A	
<400> 21	
ctagtgtatcc aaattttaca aact	24
<210> 22	
<211> 21	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> cJAK2R	
<400> 22	
gttagcaac ttcaaggtttc c	21
<210> 23	
<211> 25	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> "Sensor wt"	
<400> 23	
gtctccacag acacatactc cataa	25
<210> 24	
<211> 25	
<212> DNA	
<213> Artificial sequence	
<220>	
<223> JAK2 primer	
<400> 24	
aaaacccaaat gcttgaga aagct	25
<210> 25	
<211> 25	
<212> DNA	
<213> Artificial sequence	

<220>  
<223> Sequence of sense primer

<400> 25  
aagctttctc acaaggcattt ggttt 25

<210> 26  
<211> 26  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Sequence of antisense primer

<400> 26  
agaaaaggcat tagaaaaggct gtagtt 26

<210> 27  
<211> 17  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Sequence of "Reporter 1" (VIC)

<400> 27  
tctccacaga cacatac 17

<210> 28  
<211> 15  
<212> DNA  
<213> Artificial sequence

<220>  
<223> Sequence of "Reporter 2" (FAM)

<400> 28  
tccacagaaaa catac 15

<210> 29  
<211> 19  
<212> RNA  
<213> Artificial sequence

<220>  
<223> siRNA

<400> 29  
uggagauaugu uucugugga 19

<210> 30  
<211> 19  
<212> RNA  
<213> Artificial sequence

<220>  
<223> siRNA

<400> 30  
ggaguauguu ucuguggag

19

<210> 31  
<211> 19  
<212> RNA  
<213> Artificial sequence

<220>  
<223> siRNA

<400> 31  
gaguauguuu cuguggaga

19